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<110> Quip Technology Ltd and Imutran Ltd

<120> Porcine Retrovirus

<130> porcine retrovirus

<140> US 09/171,553

<141> 1997-04-18

<150> PCT/GB97/01087

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<150> GB9608164.1

<151> 1196-04-19

<150> GB9702668.7

<151> 1997-02-10

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<211> 524

<212> PRT

<213> Porcine retrovirus

<400> 4

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Gly	Pro	Trp	Gln	Thr	Phe	Cys	Ala	Ser	Glu	Trp	Pro	Thr	Phe	Asp	Val	35	40	45	
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Ser	Ser	Tyr	Leu	Pro	Arg	Asp	Arg	Gly	Ala	Ala	Asp	Leu	Ala	Gly	Thr	130	135	140	
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Thr	Ser	Ala	Pro	Pro	Gly	Ala	Pro	Val	Val	Glu	Gly	Pro	Ala	Ala	Gly	165	170	175	
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Gln	Pro	Leu	Gln	Tyr	Trp	Pro	Phe	Ser	Ser	Ala	Asp	Leu	Tyr	Asn	Trp	210	215	220	
Lys	Thr	Asn	His	Pro	Pro	Phe	Ser	Glu	Asp	Pro	Gln	Arg	Leu	Thr	Gly	225	230	235	240
Leu	Val	Glu	Ser	Leu	Met	Phe	Ser	His	Gln	Pro	Thr	Trp	Asp	Asp	Cys	245	250	255	

Gln Gln Leu Leu Gln Thr Leu Phe Thr Thr Glu Glu Arg Glu Arg Ile		
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Gln Leu Gln Asn Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly		
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Trp Asp Tyr Asn Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg		
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Gln Ala Leu Val Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn		
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Leu Ala Lys Val Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser		
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Val Phe Leu Glu Arg Leu Met Glu Ala Phe Arg Arg Phe Thr Pro Phe		
355	360	365
Asp Pro Thr Ser Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile		
370	375	380
Gly Gln Ser Ala Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly		
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Leu Gln Glu Ala Glu Leu Arg Asp Leu Val Arg Glu Ala Glu Lys Val		
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Tyr Tyr Arg Arg Glu Thr Glu Glu Glu Lys Glu Gln Arg Lys Glu Lys		
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Glu Arg Glu Glu Arg Glu Glu Arg Arg Asp Arg Arg Gln Glu Lys Asn		
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Leu Thr Lys Ile Leu Ala Ala Val Val Glu Gly Lys Ser Ser Arg Glu		
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Arg Glu Arg Asp Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly		
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Asn Leu Gly Asn Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys		
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Lys Glu Lys Gly His Trp Ala Arg Asn Cys Pro Lys Lys Gly Asn Lys		
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Gly Pro Lys Val Leu Ala Leu Glu Glu Asp Lys Asp
515 520

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<212> PRT
<213> Porcine retrovirus

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35 40 45
Val Met Gly Ala Thr Gly Gln Arg Gln Tyr Pro Trp Thr Thr Arg Arg
50 55 60
Thr Val Asp Leu Gly Val Gly Arg Val Thr His Ser Phe Leu Val Ile
65 70 75 80
Pro Glu Cys Pro Val Pro Leu Leu Gly Arg Asp Leu Leu Thr Lys Met
85 90 95
Gly Ala Gln Ile Ser Phe Glu Gln Gly Arg Pro Glu Val Ser Val Asn
100 105 110
Asn Lys Pro Ile Thr Val Leu Thr Leu Gln Leu Asp Asp Glu Tyr Arg
115 120 125
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130 135 140
Glu Gln Phe Pro Gln Ala Trp Ala Glu Thr Ala Gly Met Gly Leu Ala
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Lys Gln Val Pro Pro Gln Val Ile Gln Leu Lys Ala Ser Ala Thr Pro
165 170 175
Val Ser Val Arg Gln Tyr Pro Leu Ser Arg Glu Ala Arg Glu Gly Ile
180 185 190
Trp Pro His Val Gln Arg Leu Ile Gln Gln Gly Ile Leu Val Pro Val
195 200 205

Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Arg Lys Pro Gly Thr			
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Asn Asp Tyr Arg Pro Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val			
225	230	235	240
Gln Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Ala			
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Leu Pro Pro Glu Arg Asn Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala			
	260	265	270
Phe Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe			
	275	280	285
Glu Trp Arg Asp Pro Gly Thr Gly Arg Thr Gly Gln Leu Thr Trp Thr			
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Gln Val Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile			
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Pro Gly Phe Ala Thr Leu Ala Ala Pro Leu Tyr Pro Leu Thr Lys Glu			
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Lys Gly Gly Phe Ser Trp Ala Pro Glu His Gln Lys Ala Phe Asp Ala			
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Ile Lys Lys Ala Leu Leu Ser Ala Pro Ala Leu Ala Leu Pro Asp Val
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Thr Lys Pro Phe Thr Leu Tyr Val Asp Glu Arg Lys Gly Val Ala Arg
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Gly Val Leu Thr Gln Thr Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr
500 505 510

Leu Ser Lys Lys Leu Asp Pro Val Ala Ser Gly Trp Pro Val Cys Leu
515 520 525

Lys Ala Ile Ala Ala Val Ala Ile Leu Val Lys Asp Ala Asp Lys Leu
530 535 540

Thr Leu Gly Gln Asn Ile Thr Val Ile Ala Pro His Ala Leu Glu Asn
545 550 555 560

Ile Val Arg Gln Pro Pro Asp Arg Trp Met Thr Asn Ala Arg Met Thr
565 570 575

His Tyr Gln Ser Leu Leu Leu Thr Glu Arg Val Thr Phe Ala Pro Pro
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Val Thr His Asp Cys His Gln Leu Leu Ile Glu Glu Thr Gly Val Arg
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Lys Asp Leu Thr Asp Ile Pro Leu Thr Gly Glu Val Leu Thr Trp Phe
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Thr Asp Gly Ser Ser Tyr Val Val Glu Gly Lys Arg Met Ala Gly Ala
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Ala Val Val Asp Gly Thr Arg Thr Ile Trp Ala Ser Ser Leu Pro Glu
660 665 670

Gly Thr Ser Ala Gln Lys Ala Glu Leu Met Ala Leu Thr Gln Ala Leu
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Arg Leu Ala Glu Gly Lys Ser Ile Asn Ile Tyr Thr Asp Ser Arg Tyr
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Leu	Leu	Thr	Ser	Ala	Gly	Arg	Glu	Ile	Lys	Asn	Lys	Glu	Glu	Ile	Leu	725	730	735	
Ser	Leu	Leu	Glu	Ala	Leu	His	Leu	Pro	Lys	Arg	Leu	Ala	Ile	Ile	His	740	745	750	
Cys	Pro	Gly	His	Gln	Lys	Ala	Lys	Asp	Leu	Ile	Ser	Arg	Gly	Asn	Gln	755	760	765	
Met	Ala	Asp	Arg	Val	Ala	Lys	Gln	Ala	Ala	Gln	Ala	Val	Asn	Leu	Leu	770	775	780	
Pro	Ile	Ile	Glu	Thr	Pro	Lys	Ala	Pro	Glu	Pro	Arg	Arg	Gln	Tyr	Thr	785	790	795	800
Leu	Glu	Asp	Trp	Gln	Glu	Ile	Lys	Lys	Ile	Asp	Gln	Phe	Ser	Glu	Thr	805	810	815	
Pro	Glu	Gly	Thr	Cys	Tyr	Thr	Ser	Tyr	Gly	Lys	Glu	Ile	Leu	Pro	His	820	825	830	
Lys	Glu	Gly	Leu	Glu	Tyr	Val	Gln	Gln	Ile	His	Arg	Leu	Thr	His	Leu	835	840	845	
Gly	Thr	Lys	His	Leu	Gln	Gln	Leu	Val	Arg	Thr	Ser	Pro	Tyr	His	Val	850	855	860	
Leu	Arg	Leu	Pro	Gly	Val	Ala	Asp	Ser	Val	Val	Lys	His	Cys	Val	Pro	865	870	875	880
Cys	Gln	Leu	Val	Asn	Ala	Asn	Pro	Ser	Arg	Ile	Pro	Pro	Gly	Lys	Arg	885	890	895	
Leu	Arg	Gly	Ser	His	Pro	Gly	Ala	His	Trp	Glu	Val	Asp	Phe	Thr	Glu	900	905	910	
Val	Lys	Pro	Ala	Lys	Tyr	Gly	Asn	Lys	Tyr	Leu	Leu	Val	Phe	Val	Asp	915	920	925	
Thr	Phe	Ser	Gly	Trp	Val	Glu	Ala	Tyr	Pro	Thr	Lys	Lys	Glu	Thr	Ser	930	935	940	
Thr	Val	Val	Ala	Lys	Lys	Ile	Leu	Glu	Glu	Ile	Phe	Pro	Arg	Phe	Gly	945	950	955	960
Ile	Pro	Lys	Val	Ile	Gly	Ser	Asp	Asn	Gly	Pro	Ala	Phe	Val	Ala	Gln	965	970	975	

Val Ser Gln Gly Leu Ala Lys Ile Leu Gly Ile Asp Trp Lys Leu His
 980 985 990

Cys Ala Tyr Arg Pro Gln Ser Ser Gly Gln Val Glu Arg Met Asn Arg
 995 1000 1005

Thr Ile Lys Glu Thr Leu Thr Lys Leu Thr Thr Glu Thr Gly Ile Asn
 1010 1015 1020

Asp Trp Met Ala Leu Leu Pro Phe Val Leu Phe Arg Val Arg Asn Thr
 1025 1030 1035 1040

Pro Gly Gln Phe Gly Leu Thr Pro Tyr Glu Leu Leu Tyr Gly Gly Pro
 1045 1050 1055

Pro Pro Leu Ala Glu Ile Ala Phe Ala His Ser Ala Asp Val Leu Leu
 1060 1065 1070

Ser Gln Pro Leu Phe Ser Arg Leu Lys Ala Leu Glu Trp Val Arg Gln
 1075 1080 1085

Arg Ala Trp Lys Gln Leu Arg Glu Ala Tyr Ser Gly Gly Asp Leu Gln
 1090 1095 1100

Val Pro His Arg Phe Gln Val Gly Asp Ser Val Tyr Val Arg Arg His
 1105 1110 1115 1120

Arg Ala Gly Asn Leu Glu Thr Arg Trp Lys Gly Pro Tyr Leu Val Leu
 1125 1130 1135

Leu Thr Thr Pro Thr Ala Val Lys Val Glu Gly Ile Pro Thr Trp Ile
 1140 1145 1150

His Ala Ser His Val Lys Pro Ala Pro Pro Pro Asp Ser Gly Trp Arg
 1155 1160 1165

Ala Glu Lys Thr Glu Asn Pro Leu Lys Leu Arg Leu His Arg Leu Val
 1170 1175 1180

Pro Tyr Ser Asn Asn Asn Ser Pro Gly Gln
 1185 1190

<210> 6

<211> 656

<212> PRT

<213> Porcine retrovirus

<400> 6

Met His Pro Thr Leu Ser Arg Arg His Leu Pro Thr Arg Gly Gly Glu
1 5 10 15

Pro Lys Arg Leu Arg Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
20 25 30

Leu Thr Leu Thr Ile Thr Pro Gln Ala Ser Ser Lys Arg Leu Ile Asp
35 40 45

Ser Ser Asn Pro His Arg Pro Leu Ser Leu Thr Trp Leu Ile Ile Asp
50 55 60

Pro Asp Thr Gly Val Thr Val Asn Ser Thr Arg Gly Val Ala Pro Arg
65 70 75 80

Gly Thr Trp Trp Pro Glu Leu His Phe Cys Leu Arg Leu Ile Asn Pro
85 90 95

Ala Val Lys Ser Thr Pro Pro Asn Leu Val Arg Ser Tyr Gly Phe Tyr
100 105 110

Cys Cys Pro Gly Thr Glu Lys Glu Lys Tyr Cys Gly Gly Ser Gly Glu
115 120 125

Ser Phe Cys Arg Arg Trp Ser Cys Val Thr Ser Asn Asp Gly Asp Trp
130 135 140

Lys Trp Pro Ile Ser Leu Gln Asp Arg Val Lys Phe Ser Phe Val Asn
145 150 155 160

Ser Gly Pro Gly Lys Tyr Lys Met Met Lys Leu Tyr Lys Asp Lys Ser
165 170 175

Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser Phe Thr Glu Arg
180 185 190

Lys Thr Gly Lys Tyr Ser Lys Val Asp Lys Trp Tyr Glu Leu Gly Asn
195 200 205

Ser Phe Leu Leu Tyr Gly Gly Gly Ala Gly Ser Thr Leu Thr Ile Arg
210 215 220

Leu Arg Ile Glu Thr Gly Thr Glu Pro Pro Val Ala Met Gly Pro Asp
225 230 235 240

Lys Val Leu Ala Glu Gln Gly Pro Pro Ala Leu Glu Pro Pro His Asn

245								250					255			
Leu	Pro	Val	Pro	Gln	Leu	Thr	Ser	Leu	Arg	Pro	Asp	Ile	Thr	Gln	Pro	
260								265				270				
Pro	Ser	Asn	Ser	Thr	Thr	Gly	Leu	Ile	Pro	Thr	Asn	Thr	Pro	Arg	Asn	
275								280				285				
Ser	Pro	Gly	Val	Pro	Val	Lys	Thr	Gly	Gln	Arg	Leu	Phe	Ser	Leu	Ile	
290								295				300				
Gln	Gly	Ala	Phe	Gln	Ala	Ile	Asn	Ser	Thr	Asp	Pro	Asp	Ala	Thr	Ser	
305				310				315				320				
Ser	Cys	Trp	Leu	Cys	Leu	Ser	Ser	Gly	Pro	Pro	Tyr	Tyr	Glu	Gly	Met	
				325				330				335				
Ala	Lys	Glu	Arg	Lys	Phe	Asn	Val	Thr	Lys	Glu	His	Arg	Asn	Gln	Cys	
340								345				350				
Thr	Trp	Gly	Ser	Arg	Asn	Lys	Leu	Thr	Leu	Thr	Glu	Val	Ser	Gly	Lys	
355								360				365				
Gly	Thr	Cys	Ile	Gly	Lys	Ala	Pro	Pro	Ser	His	Gln	His	Leu	Cys	Tyr	
370								375				380				
Ser	Thr	Val	Val	Tyr	Glu	Gln	Ala	Ser	Glu	Asn	Gln	Tyr	Leu	Val	Pro	
385				390				395				400				
Gly	Tyr	Asn	Arg	Trp	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Val	
				405				410				415				
Ser	Thr	Ser	Val	Phe	Asn	Gln	Ser	Lys	Asp	Phe	Cys	Val	Met	Val	Gln	
420								425				430				
Ile	Val	Pro	Arg	Val	Tyr	Tyr	His	Pro	Glu	Glu	Val	Val	Leu	Asp	Glu	
435								440				445				
Tyr	Asp	Tyr	Arg	Tyr	Asn	Arg	Pro	Lys	Arg	Glu	Pro	Val	Ser	Leu	Thr	
450								455				460				
Leu	Ala	Val	Met	Leu	Gly	Leu	Gly	Thr	Ala	Val	Gly	Val	Gly	Thr	Gly	
465				470				475				480				
Thr	Ala	Ala	Leu	Ile	Thr	Gly	Pro	Gln	Gln	Leu	Glu	Lys	Gly	Leu	Gly	
				485				490				495				
Glu	Leu	His	Ala	Ala	Met	Thr	Glu	Asp	Leu	Arg	Ala	Leu	Lys	Glu	Ser	

500	505	510
Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val Val Leu		
515	520	525
Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Arg Glu Gly Gly Leu		
530	535	540
Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val Asp His Ser Gly		
545	550	555
Ala Ile Arg Asp Ser Met Asn Lys Leu Arg Lys Lys Leu Glu Arg Arg		
565	570	575
Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu Gly Trp Phe Asn		
580	585	590
Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu Thr Gly Pro Leu		
595	600	605
Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys Leu Ile Asn Arg		
610	615	620
Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val Gln Ile Met Val		
625	630	635
Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly Glu Thr Asp Leu		
645	650	655

<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:OLIGONUCLEOTIDE
DESIGNED AGAINST PORCINE RETROVIRUS GENOME

<400> 7

ggaagtggac ttcactga

18

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:OLIGONUCLEOTIDE
DESIGNED AGAINST PORCINE RETROVIRUS GENOME

<400> 8

ctttccaccc cgaatcgg

18

<210> 9

<211> 1974

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:GENOMIC "RAJI"
CLONE DNA ENV REGION

<400> 9

atgcatccca cgtaaagctg gcgccacctc ccgactcggg gtggagagcc gaaaagactg 60
agaateccct taagcttcgc ctccatcgcc tgggttcctta ctctaacaat aactccccag 120
gccagtagta aacgccttat agacagctcg aacccccata gacctttatc ccctacctgg 180
ctgattattg accctgatac ggggtgtcact gtaaatagca ctcgaggtgt tgctcctaga 240
ggcacctggg ggccctgaact gcattttctgc ctccgattga ttaaccccg cgttaaaaagc 300
acacctccca acctagtccg tagttatggg ttctattgct gcccaggcac agagaaagag 360
aaatactgtg ggggttctgg ggaatccttc tgtaggagat ggagctgcgt cacctccaac 420
gatggagact ggaaatggcc gatctctctc caggaccggg taaaattctc ctttgtcaat 480
tccggccccg gcaagtacaa aatgatgaaa ctatataaag ataagagctg ctccccatca 540
gacttagatt atctaaagat aagtttctact gaaaaaggaa aacaggaaaa tattcaaaag 600
tgataaaatg gtatgagctg gggaatagtt ttttataaat atggcggggg agcagggtcc 660
actttaacca ttgccttag gatagagacg gggacagaac cccctgtggc aatgggaccc 720
gataaagtac tggctgaaca ggggcccccg gccctggagc caccgcataa cttgccggtg 780
ccccaatata cctcgtctgc gcctgacata acacagccgc ctagcaacag taccactgga 840
ttgattccta ccaacacgcc tagaaactcc ccagggtgtc ctgttaagac aggacagaga 900
ctcttcagtc tcatccaggg agctttccaa gccatcaact ccaccgaccc tgatgccact 960
tcttcttggt ggctttgtct atcctcaggg cctccttatt atgaggggat ggctaaagaa 1020
agaaaattca atgtgaccaa agagcataga aatcaatgta catgggggtc ccgaaataag 1080
cttaccctca ctgaagtttc cgggaagggg acatgcatag gaaaagctcc cccatcccac 1140
caacaccttt gctatagtac tgtggtttat gagcaggcct cagaaaaatca gtatttagta 1200
cctggttata acagggtggg ggcattgcaat actgggttaa cccctgtgt ttccacctca 1260
gtcttcaacc aatccaaaga tttgtgtgtc atggtccaaa tcgtcccccg agtgtactac 1320
catcctgagg aagtggctct tgatgaatat gactatcggg ataaccgacc aaaaagagaa 1380
cccgtatccc ttaccctagc tgtaatgtc ggattaggga cggccgttg cgtaggaaca 1440
gggacagctg ccctgatcac aggaccacag cagctagaga aaggacttgg tgagctacat 1500
gcggccatga cagaagatct ccgagcctta aaggagtctg ttagcaacct agaagagtcc 1560
ctgacttctt tgtctgaagt ggttctacag aaccggaggg gattagatct gctgtttcta 1620

agagaaggtg gggttatgtgc agccttaaaa gaagaatggt gcttctatgt agatcactca 1680
 ggagccatca gagactccat gaacaagctt agaaaaaagt tagagaggcg tcgaagggaa 1740
 agagaggctg accaggggtg gtttgaagga tggttcaaca ggtctccttg gatgaccacc 1800
 ctgctttctg ctctgacggg gccctagta gtcctgctcc tgttacttac agttgggcct 1860
 tgcttaatta ataggtttgt tgcctttggt agagaacgag tgagtgcagt ccagatcatg 1920
 gtacttaggc aacagtacca aggccttctg agccaaggag aaactgacct ctag 1974

<210> 10

<211> 657

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:AMINO ACID

SEQUENCE OF ENV REGION OF "RAJI"

<400> 10

Met	His	Pro	Thr	Leu	Ser	Trp	Arg	His	Leu	Pro	Thr	Arg	Gly	Gly	Glu
1				5					10					15	

Pro	Lys	Arg	Leu	Arg	Ile	Pro	Leu	Ser	Phe	Ala	Ser	Ile	Ala	Trp	Phe
			20					25					30		

Leu	Thr	Leu	Thr	Ile	Thr	Pro	Gln	Ala	Ser	Ser	Lys	Arg	Leu	Ile	Asp
	35					40					45				

Ser	Ser	Asn	Pro	His	Arg	Pro	Leu	Ser	Pro	Thr	Trp	Leu	Ile	Ile	Asp
	50					55					60				

Pro	Asp	Thr	Gly	Val	Thr	Val	Asn	Ser	Thr	Arg	Gly	Val	Ala	Pro	Arg
	65				70					75				80	

Gly	Thr	Trp	Trp	Pro	Glu	Leu	His	Phe	Cys	Leu	Arg	Leu	Ile	Asn	Pro
				85					90					95	

Ala	Val	Lys	Ser	Thr	Pro	Pro	Asn	Leu	Val	Arg	Ser	Tyr	Gly	Phe	Tyr
		100						105					110		

Cys	Cys	Pro	Gly	Thr	Glu	Lys	Glu	Lys	Tyr	Cys	Gly	Gly	Ser	Gly	Glu
		115					120					125			

Ser	Phe	Cys	Arg	Arg	Trp	Ser	Cys	Val	Thr	Ser	Asn	Asp	Gly	Asp	Trp
	130					135					140				

Lys	Trp	Pro	Ile	Ser	Leu	Gln	Asp	Arg	Val	Lys	Phe	Ser	Phe	Val	Asn
145					150					155				160	

Ser Gly Pro Gly Lys Tyr Lys Met Met Lys Leu Tyr Lys Asp Lys Ser	165	170	175
Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser Phe Thr Glu Lys	180	185	190
Gly Lys Gln Glu Asn Ile Gln Lys Trp Ile Asn Gly Met Ser Trp Gly	195	200	205
Ile Val Phe Tyr Lys Tyr Gly Gly Gly Ala Gly Ser Thr Leu Thr Ile	210	215	220
Arg Leu Arg Ile Glu Thr Gly Thr Glu Pro Pro Val Ala Met Gly Pro	225	230	235
Asp Lys Val Leu Ala Glu Gln Gly Pro Pro Ala Leu Glu Pro Pro His	245	250	255
Asn Leu Pro Val Pro Gln Leu Thr Ser Leu Arg Pro Asp Ile Thr Gln	260	265	270
Pro Pro Ser Asn Ser Thr Thr Gly Leu Ile Pro Thr Asn Thr Pro Arg	275	280	285
Asn Ser Pro Gly Val Pro Val Lys Thr Gly Gln Arg Leu Phe Ser Leu	290	295	300
Ile Gln Gly Ala Phe Gln Ala Ile Asn Ser Thr Asp Pro Asp Ala Thr	305	310	315
Ser Ser Cys Trp Leu Cys Leu Ser Ser Gly Pro Pro Tyr Tyr Glu Gly	325	330	335
Met Ala Lys Glu Arg Lys Phe Asn Val Thr Lys Glu His Arg Asn Gln	340	345	350
Cys Thr Trp Gly Ser Arg Asn Lys Leu Thr Leu Thr Glu Val Ser Gly	355	360	365
Lys Gly Thr Cys Ile Gly Lys Ala Pro Pro Ser His Gln His Leu Cys	370	375	380
Tyr Ser Thr Val Val Tyr Glu Gln Ala Ser Glu Asn Gln Tyr Leu Val	385	390	395
Pro Gly Tyr Asn Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys	405	410	415

Val Ser Thr Ser Val Phe Asn Gln Ser Lys Asp Leu Cys Val Met Val
420 425 430

Gln Ile Val Pro Arg Val Tyr Tyr His Pro Glu Glu Val Val Leu Asp
435 440 445

Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro Val Ser Leu
450 455 460

Thr Leu Ala Val Met Leu Gly Leu Gly Thr Ala Val Gly Val Gly Thr
465 470 475 480

Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu Lys Gly Leu
485 490 495

Gly Glu Leu His Ala Ala Met Thr Glu Asp Leu Arg Ala Leu Lys Glu
500 505 510

Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val Val
515 520 525

Leu Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Arg Glu Gly Gly
530 535 540

Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val Asp His Ser
545 550 555 560

Gly Ala Ile Arg Asp Ser Met Asn Lys Leu Arg Lys Lys Leu Glu Arg
565 570 575

Arg Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu Gly Trp Phe
580 585 590

Asn Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu Thr Gly Pro
595 600 605

Leu Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys Leu Ile Asn
610 615 620

Arg Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val Gln Ile Met
625 630 635 640

Val Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly Glu Thr Asp
645 650 655

Leu